```
GAATTCGGCACGAGGTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCC
1   ---------+---------+---------+---------+---------+---------+ 60

ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
61  ---------+---------+---------+---------+---------+---------+ 120

AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300

CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+ 360

CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+ 420

GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+ 480

TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+ 540

ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+ 600

CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+ 660

CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+ 720

CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
721 ---------+---------+---------+---------+---------+---------+ 780

GACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG
781 ---------+---------+---------+---------+---------+---------+ 840
```

FIG. 1A1

```
                                                                    CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC
841 ---------+---------+---------+---------+---------+---------+ 900

    TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC
901 ---------+---------+---------+---------+---------+---------+ 960

    ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG
961 ---------+---------+---------+---------+---------+---------+ 1020

    GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA
1021 ---------+---------+---------+---------+---------+---------+ 1080

    GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC
1081 ---------+---------+---------+---------+---------+---------+ 1140

    GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

    CGGTGTACGTGGTTGTGGCCAGTCCCCTCGATGTGAACAAGAACGGCTGGACCCATGTGT
1201 ---------+---------+---------+---------+---------+---------+ 1260

    GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

    AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

    AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

    ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

    TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560

    GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561 ---------+---------+---------+---------+---------+---------+ 1620

    GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621 ---------+---------+---------+---------+---------+---------+ 1680
```

FIG. 1A2

```
      GTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681  ---------+---------+---------+---------+---------+---------+ 1740

      GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741  ---------+---------+---------+---------+---------+---------+ 1800

      CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801  ---------+---------+---------+---------+---------+---------+ 1860

      GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861  ---------+---------+---------+---------+---------+---------+ 1920

      AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921  ---------+---------+---------+---------+---------+---------+ 1980

      TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401  ---------+---------+---------+---------+---------+---------+ 2460

      TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461  ---------+---------+---------+---------+-------- 2508
```

FIG. 1A3

```
   1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCCATCCGAAAG   69
  70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA  138
 139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC  207
 208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC  276
 277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC  345
 346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC  414
 415 TGCCGGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC  483
 484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCATCACCCCCGTC  552
 553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCAGCAACCCCATC  621
 622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGCACACCGACTCC  690
 691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCG  759
 760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTT  828
 829 GTGTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT  897
 898 CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG  966
 967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035
1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104
1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173
1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242
1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311
1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCAGGCTTCTATGGTAAA 1380
1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449
1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518
1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587
1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656
1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725
1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794
```

FIG. 1B1

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863
1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932
1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001
2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCACCAGCCCGAGGCCTGCAGGAGTGAAACGGAGACCATG 2070
2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139
2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208
2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277
2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346
2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415
2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484
2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553
2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622
2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691
2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760
2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829
2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGGCAAAGCTT 2883

FIG. 1B2

```
  1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
 61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV
```

FIG. 2

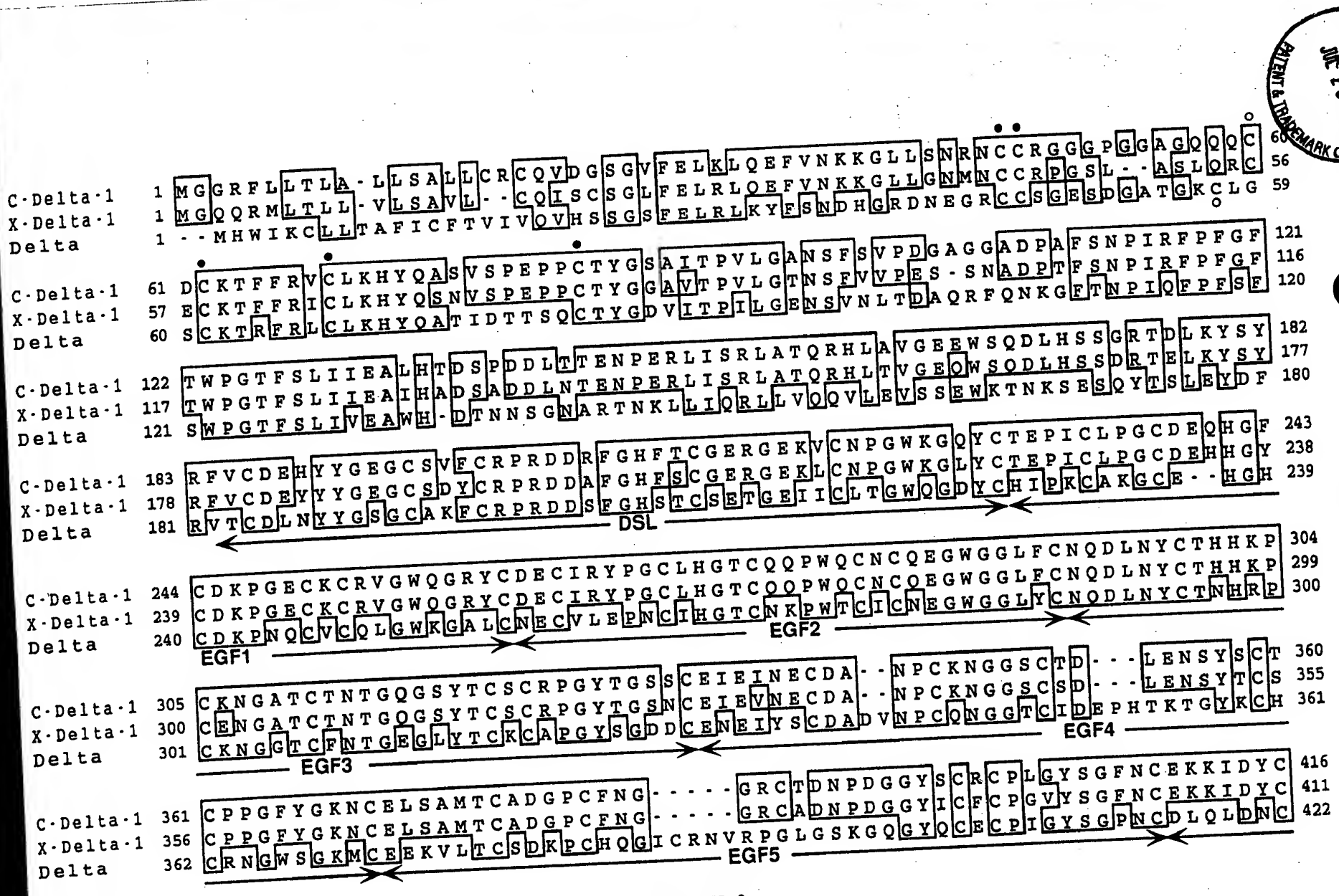

FIG. 3A

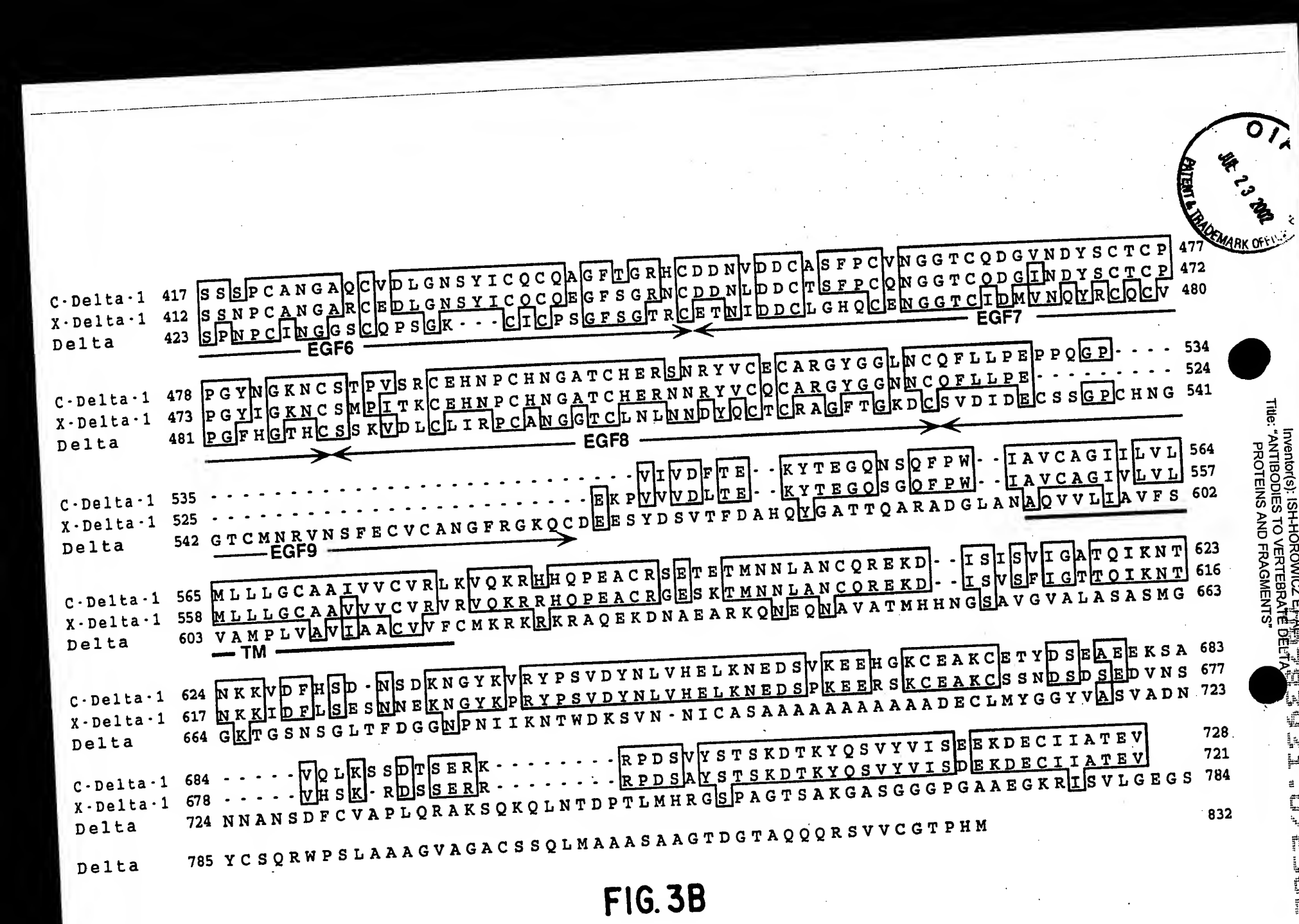

FIG. 3B

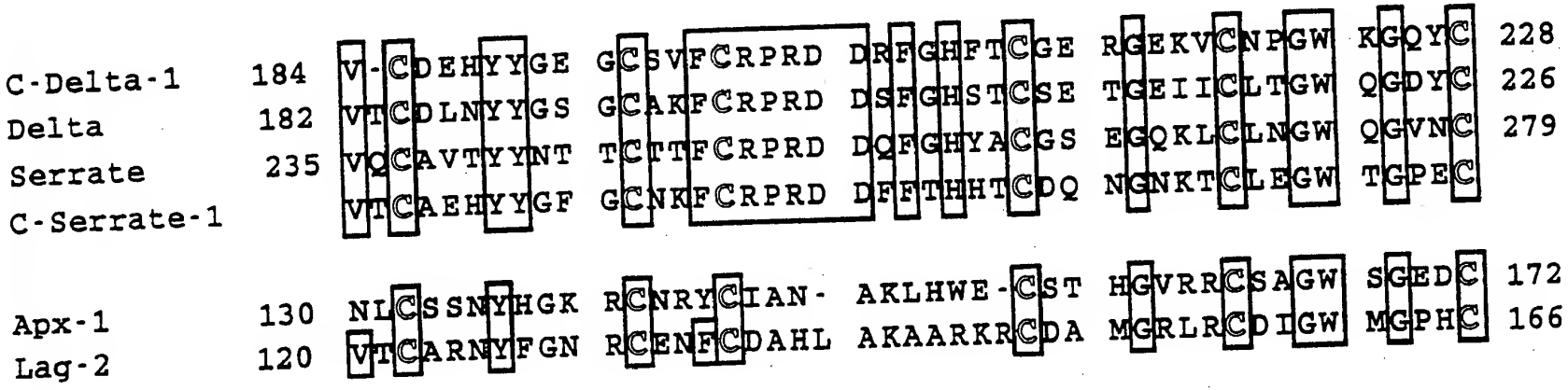

FIG. 4

FIG.5A

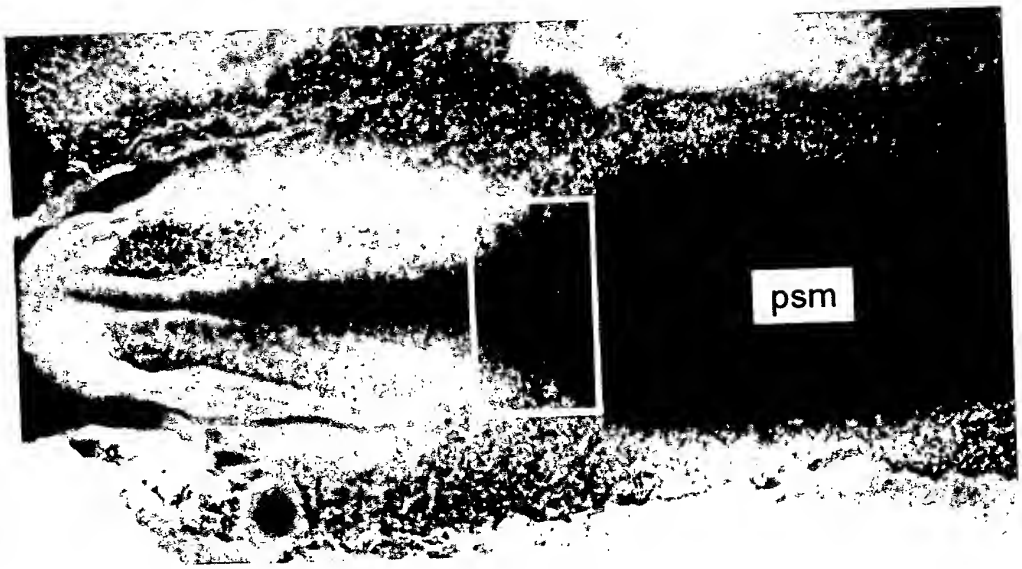

FIG.5B

FIG.5C

FIG.5D

FIG.5E

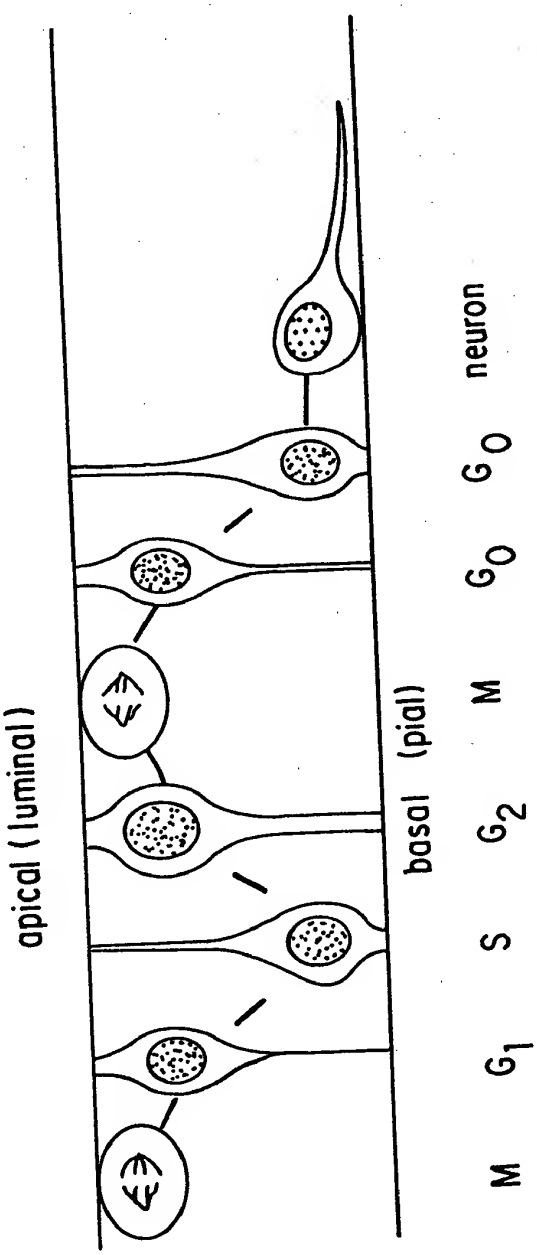

FIG. 6A

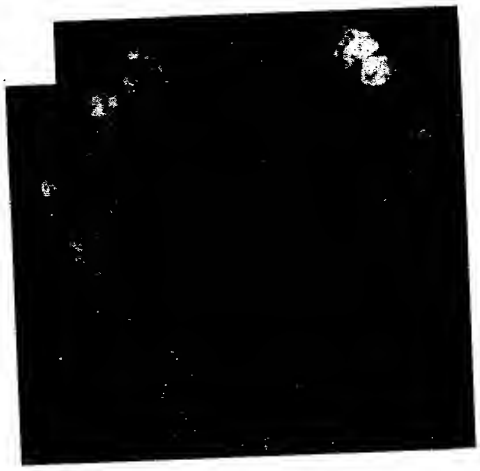

FIG.6B

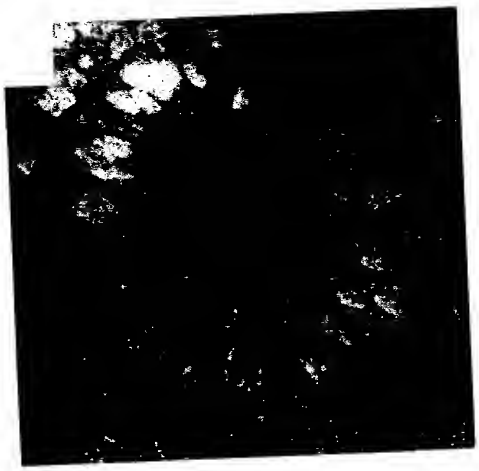

FIG.6C

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT     60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG    120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT    180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC    240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC    300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC    360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC    420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG    480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC    540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG    600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG    660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT    720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG    780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA    840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC    900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG    960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT   1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC   1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT   1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC   1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC   1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG   1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC   1380
```

FIG. 7A

```
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA   1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC   1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC   1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG   1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT   1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC   1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC   1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT   1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG   1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA   1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC   2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA   2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG   2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA   2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA   2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT   2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT   2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG   2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT   2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG   2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA   2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT            2692
```

FIG. 7B

```
MGRRSALALA VVSALLCQVW SSGVFELKLQ EFVNKKGLLG NRNCCRGGSG      50
PPCACRTFFR VCLKHYQASV SPEPPCTYGS AVTPVLGVDS FSLPDGAGID     100
PAFSNPIRFP FGFTWPGTFS LIIEALHTDS PDDLATENPE RLISRLTTQR     150
HLTVGEEWSQ DLHSSGRTDL RYSYRFVCDE HYYGEGCSVF CRPRDDAFGH     200
FTCGDRGEKM CDPGWKGQYC TDPICLPGCD DQHGYCDKPG ECKCRVGWQG     250
RYCDECIRYP GCLHGTCQQP WQCNCQEGWG GLFCNQDLNY CTHHKPCRNG     300
ATCTNTGQGS YTCSCRPGYT GANCELEVDE CAPSPCKNGA SCTDLEDSFS     350
CTCPPGFYGK VCELSAMTCA DGPCFNGGRC SDNPDGGYTC HCPLGFSGFN     400
CEKKMDLCGS SPCSNGAKCV DLGNSYLCRC QAGFSGRYCE DNVDDCASSP     450
CANGGTCRDS VNDFSCTCPP GYTGKNCSAP VSRCEHAPCH NGATCHQRGQ     500
RYMCECAQGY GGPNCQFLLP EPPPGPMVVD LSERHMESQG GPFPWVAVCA     550
GVVLVLLLLL GCAAVVVCVR LKLQKHQPPP EPCGGETETM NNLANCQREK     600
DVSVSIIGAT QIKNTNKKAD FHGDHGAEKS SFKVRYPTVD YNLVRDLKGD     650
EATVRDTHSK RDTKCQSQSS AGEEKIAPTL RGGEIPDRKR PESVYSTSKD     700
TKYQSVYVLS AEKDECVIAT EV                                   722
```

FIG. 8

```
CHICK DELTA       MGGRFLLTLA LLSALLGRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG  50
MOUSE DELTA.PEP   MGRRSALALA VVSALLCQ-- VWSSGVFELK LQEFVNKKGL LGNRNCCRGG  48

CONSENSUS         MG.R..L.LA ..SALLC... V..SGVFELD LQEFVNKKGL L.NRNCCRGG  50

CHICK DELTA       GPGGAGQQQC DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV 100
MOUSE DELTA.PEP   --SGP--PC ACRTFFRVCL KHYQASVSPE PPCTYGSAVT PVLGVDSFSL  93

CONSENSUS         ...G.....C ..C.TFFRVCL KHYQASVSPE PPCTYGSA.T PVLG..SFS. 100

CHICK DELTA       PDGAGGADPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLPTENPERL 150
MOUSE DELTA.PEP   PDGAG-IDPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLATENPERL 142

CONSENSUS         PDGAG..DPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DL.TENPERL 150

CHICK DELTA       ISRLATQRHL AVGEEWSQDL HSSGRTDLKY SYRFVCDEHY YGEGCSVFCR 200
MOUSE DELTA.PEP   ISRLTTQRHL TVGEEWSQDL HSSGRTDLRY SYRFVCDEHY YGEGCSVFCR 192

CONSENSUS         ISRL.TQRHL .VGEEWSQDL HSSGRTDL.Y SYRFVCDEHY YGEGCSVFCR 200

CHICK DELTA       PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ HGFCDKPGEC 250
MOUSE DELTA.PEP   PRDDAFGHFT CGDRGEKMCD PGWKGQYCTD PICLPGCDDQ HGYCDKPGEC 242

CONSENSUS         PRDD.FGHFT CG.RGEK.C. PGWKGQYCT. PICLPGCD.Q HG.CDKPGEC 250

CHICK DELTA       KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300
MOUSE DELTA       KCRVGWQGRY CDECIRYPGC LHFTCQQPWQ CNCQEGWGGL FCNQDLNYCT 292

CONSENSUS         KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300

CHICK DELTA       HHKPCKNGAT CTNTGQGSTY CSCRPGYTGS SCEIEINECD ANPCKNGGSC 350
MOUSE DELTA.PEP   HHKPCRNGAT CTNTGQGSYT CSCRPGYTGA NCELEVDECA PSPCKNGASC 342

CONSENSUS         HHKPC.NGAT CTNTGQGSYT CSCRPGYTG. .CE.E..EC. ..PCKNG.SC 350

CHICK DELTA       TDLENSYSCT CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC 400
MOUSE DELTA.PEP   TDLEDSFSCT CPPGFYGKVC ELSAMTCADG PCFNGGRCSD NPDGGYTCHC 392

CONSENSUS         TDLE.S.SCT CPPGFYGK.C ELSAMTCADG PCFNGGRC.D NPDGGY.C.C 400

CHICK DELTA       PLGYSGFNCE KKIDYCSSSP CANGAQCVDL GNSYICQCQA GFTGRHCDDN 450
MOUSE DELTA.PEP   PLGFSGFNCE KKMDLCGSSP CSNGAKCVDL GNSYLCRCQA GFSGRYCEDN 442

CONSENSUS         PLG.SGFNCE KK.D.C.SSP C.NGA.CVDL GNSY.C.CQA GF.GR.C.DN 450
```

FIG.9A

```
CHICK DELTA       VDDCASFPQV NGGTCQDGVN DYSCTCPPGY NGKNCSTPVS RCEHNPCHNG 500
MOUSE DELTA.PEP   VDDCASSPQA NGGTCRDSVN DFSCTCPPGY TGKNCSAPVS RCEHAPCHNG 492

CONSENSUS         VDDCAS.PQ. NGGTC.D.VN D.SCTCPPGY .GKNCS.PVS RCEH.PCHNG 500

CHICK DELTA       ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT EKYTEGQNSQ 550
MOUSE DELTA       ATCHQRGQRY MCECAQGYGG PNCQFLLPEP PPGPMVVDLS ERHMESQGGP 542

CONSENSUS         ATCH.R..RY .CECA.GYGG .NCQFLLPEP P.GP..VD.. E...E.Q... 550

CHICK DELTA       FPWIAVCAGI ILVLMLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN 600
MOUSE DELTA.PEP   FPWVAVCAGV VLVLLLLGC AAVVVCVRLK LQKHQPPPEP CGGETETMNN 592

CONSENSUS         FPW.AVCAG. .LVL.LLGC AA.VVCVRLK .QK....PE. C..ETETMNN 600

CHICK DELTA       LANCQREKDI SISVIGATQI KNTNKKVDFH SDN-SDKNGY KVRYPSVDYN 649
MOUSE DELTA       LANCQREKDV SVSIIGATQI KNTNKKADFH GDHGAEKSSF KVRYPTVDYN 642

CONSENSUS         LANCQREKD. S.S.IGATQI KNTNKK.DFH .D....K... KVRYP.VDYN 650

CHICK DELTA       LVHELKNED- SVKEEHGKCE AKCETYDSEA EEKSAVQLKS SDTSERKRPD 698
MOUSE DELTA.PEP   LVRDLKGDEA TVRDTHSKRD TKCQSQSSAG EEKIAPTLRG GEIPDRKRPE 692

CONSENSUS         LV..LK.... .M...H.K.. .KC....S. EEK.A..L.. .....RKRP. 700

CHICK DELTA       SVYSTSKDTK YQSVYVISEE KDECIIATEV 728
MOUSE DELTA.PEP   SVYSTSKDTK YQSVYVLSAE KDECVIATEV 722
CONSENSUS         SVYSTSKDTK YQSVYV.S.E KDEC.IATEV 730
```

FIG.9B

```
        10          20          30          40          50          60
                    *           *           *           *           *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TCAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y D E  X P G E  L P A  * E G  H L S Q  H H R>
  T M N  N L A  N C Q  R E K  D I S V  S I I  G>
   R * X  T W R  T A S  V R R  T S Q  S A S  S>

        70          80          90          100         110         120
                    *           *           *           *           *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G X V  R S X  T P T  R R T  X X R  G T X  A>
  A T S  D Q E  H Q Q  E G L  X X G  G P X  R>
G X R Q  I X N  T N K  K A D  F X X  G D X  S>

        130         140         150         160         170         180
                    *           *           *           *           *
TCCGACAAGA ATGGMTTTCA AGGCCYGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S D K  N G F  Q G P  L P Q  R G L  * L V  Q D>
  P T R  M X F  K A R  Y P S  V D Y  N S C  R T>
V R Q E  W X S  R P A  T P A  W T I  T R A  G>

        190         200         210         220         230         240
                    *           *           *           *           *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L K G  D D T A  V R T  S H S  K R D  T K C  Q>
  S R V  T T P  P S G  R R T  A S V  T P S  A S>
P Q G *  R H R  R Q D  V A Q  Q A *  H Q V  P>

        250         260         270         280         290         300
                    *           *           *           *           *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S P G  S S G R  R R G  P R P  H S G X  A C C>
  P Q A  P Q G  G E G D  P D H  T Q G  X R A  A>
V P R L  L R E  E K G  T P T T  L R G  C V L>

        310         320         330         340         350         360
                    *           *           *           *           *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G P G  S G G G  T W G  V S S  W N H C  S V S>
  G R A  Q E G  V P G G  C L P  G T T  A P F  L>
R A G L  R R G  Y L G  G V F L  E P L  L R F>
```

FIG. 10A

```
      370        380        390        400        410        420
                  *                     *                     *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K  C  S  H  A  F  I  V  D  F  L  Y  F  P  F  S  G  E>
  F  P  N  V  L  M  H  S  L  W  I  F  S  I  F  L  L  V  E  K>
S  S  Q  M  F  S  C  I  H  C  G  F  S  L  F  S  F  *  W  R>

      430        440        450        460        470        480
                  *                     *                     *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E  R  K  R  P  D  S  G  C  S  T  S  K  D  T  K  Y  Q>
  H  L  K  E  K  G  R  T  R  A  V  Q  L  Q  K  T  P  S  T  S>
S  I  *  K  K  K  A  G  L  G  L  F  N  F  K  R  H  Q  V  P>

      490        500        510        520
                  *                     *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y  V  I  S  E  E  K  D  E  C  V  I  A>
  R  C  T  S  Y  P  R  R  R  T  S  A  S  S>
V  G  V  R  H  I  R  G  E  G  R  V  R  H  R>
```

FIG. 10B

```
  1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY  50
    |||||||||||||||:|:||||||||||||.|| ::   |||||: |.||
597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643

 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
    ||||||||::||.:| .|:..|:| :.||: .:|.:  :::
644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA........  683

101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                |::    |::.||||||||.
684 ............................VQLK....SSDTSERKRPDSV 700

151 CSTSKDTKYQSVYVISEEKDECVIA  175
    :||||||||||||||||||||:||
701 YSTSKDTKYQSVYVISEEKDECIIA  725
```

FIG.11

```
          10         20         30         40         50         60
      *   *   *   *   *   *   *   *   *   *   *   *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
          70         80         90        100        110        120
      *   *   *   *   *   *   *   *   *   *   *   *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
         130        140        150        160        170        180
      *   *   *   *   *   *   *   *   *   *   *   *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
         190        200        210        220        230        240
      *   *   *   *   *   *   *   *   *   *   *   *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
         250        260        270        280        290        300
      *   *   *   *   *   *   *   *   *   *   *   *
CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
         310        320        330        340        350        360
      *   *   *   *   *   *   *   *   *   *   *   *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
         370        380        390        400        410        420
      *   *   *   *   *   *   *   *   *   *   *   *
CCCTGGCTCG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
         430        440        450        460        470        480
      *   *   *   *   *   *   *   *   *   *   *   *
GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
         490        500        510        520        530        540
      *   *   *   *   *   *   *   *   *   *   *   *
GTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
         550        560        570        580        590        600
      *   *   *   *   *   *   *   *   *   *   *   *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
         610        620        630        640        650        660
      *   *   *   *   *   *   *   *   *   *   *   *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
         670        680        690        700        710        720
      *   *   *   *   *   *   *   *   *   *   *   *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
         730        740        750        760        770        780
      *   *   *   *   *   *   *   *   *   *   *   *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
         790        800        810        820        830        840
      *   *   *   *   *   *   *   *   *   *   *   *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
         850        860        870        880        890        900
      *   *   *   *   *   *   *   *   *   *   *   *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A1

```
          910         920         930         940         950         960
      *   *   *   *   *   *   *   *   *   *   *   *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
          970         980         990        1000        1010        1020
      *   *   *   *   *   *   *   *   *   *   *   *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
         1030        1040        1050        1060        1070        1080
      *   *   *   *   *   *   *   *   *   *   *   *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
         1090        1100        1110        1120        1130        1140
      *   *   *   *   *   *   *   *   *   *   *   *
TCCTCCCCGT GCGCCAACGG ACCTCGGTGA CGGGATGGCG TGAACGACTT CTCCTGCACC
         1150        1160        1170        1180        1190        1200
      *   *   *   *   *   *   *   *   *   *   *   *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACCTG CGAGCACGCA
         1210        1220        1230        1240        1250        1260
      *   *   *   *   *   *   *   *   *   *   *   *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGCACGCA
         1270        1280        1290        1300        1310        1320
      *   *   *   *   *   *   *   *   *   *   *   *
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCC AAACTGCCCC CCCGGCCCCA
         1330        1340        1350        1360        1370        1380
      *   *   *   *   *   *   *   *   *   *   *   *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
         1390        1400        1410        1420        1430        1440
      *   *   *   *   *   *   *   *   *   *   *   *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTG CCGCTGTGGT
         1450        1460        1470        1480        1490        1500
      *   *   *   *   *   *   *   *   *   *   *   *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
         1510        1520        1530        1540        1550        1560
      *   *   *   *   *   *   *   *   *   *   *   *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
         1570        1580        1590        1600        1610        1620
      *   *   *   *   *   *   *   *   *   *   *   *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
         1630        1640        1650        1660        1670        1680
      *   *   *   *   *   *   *   *   *   *   *   *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
         1690        1700        1710        1720        1730        1740
      *   *   *   *   *   *   *   *   *   *   *   *
CCTCAAGGGT GACGACACCG CCGTCAGCCA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
         1750        1760        1770        1780        1790        1800
      *   *   *   *   *   *   *   *   *   *   *   *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
```

FIG.12A2

```
     1810        1820        1830        1840        1850        1860
      *   *       *   *       *   *       *   *       *   *       *   *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
     1870        1880        1890        1900        1910        1920
      *   *       *   *       *   *       *   *       *   *       *   *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
     1930        1940        1950        1960        1970        1980
      *   *       *   *       *   *       *   *       *   *       *   *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT

T
```

FIG. 12A3

```
          10        20        30        40        50        60
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  a.a.no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
H  W  V  R  A  P  L  E  V  D  G  I  D  K  L  D  I  E  F  R>      20
 I  G  Y  G  P  P  S  R  S  T  V  S  I  S  L  I  S  N  S [G>]    20
  L  G  T  G  P  P  R  G  R  R  Y  R  *  A  *  Y  R  I  P>      19

          70        80        90        100       110       120
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L  H  L  A  G  H  L  L  S  D  Y  *  S  S  P  H  R  F  S  *>     40
[F  T  W  P  G  T  F  S  L  I  I  E  A  L  H  T  D  S  P  D>]   40
A  S  P  G  R  A  P  S  L  *  L  L  K  L  S  T  Q  I  L  L>     39

          130       140       150       160       170       180
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 *  P  R  N  R  K  P  R  K  T  H  Q  P  P  G  H  P  E  A  P>     60
[D  L  A  T  E  N  P  E  R  L  I  S  R  L  A  T  Q  R  H  L>]   60
M  T  S  Q  Q  K  T  Q  K  D  S  S  A  A  W  P  P  R  G  T>     59

          190       200       210       220       230       240
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D  G  G  R  G  V  V  P  G  P  A  Q  Q  R  P  H  G  P  Q  V>     80
[T  V  G  E  E  W  S  Q  D  L  H  S  S  G  R  T  D  L  K  Y>]   80
 *  R  W  A  R  S  G  P  R  T  C  T  A  A  A  A  R  T  S  S>     79

          250       260       270       280       290       300
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L  L  P  L  R  V  *  R  T  L  L  R  R  G  L  L  R  F  L  P>     100
[S  Y  R  F  V  C  D  E  H  Y  Y  G  E  G  C  S  V  F  C  R>]   100
T  P  T  A  S  C  V  T  N  T  T  T  E  R  A  A  P  F  S  A>     99

          310       320       330       340       350       360
          *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S  P  G  R  C  L  R  P  L  H  L  W  G  A  W  G  E  S  V  Q>     120
[P  R  D  D  A  F  G  H  F  T  C  G  E  R  G  E  K  V  C  N>]   120
V  P  G  T  M  P  S  A  T  S  P  V  C  S  V  G  R  K  C  A>     119
```

FIG.12B1

```
          370        380        390        400        410        420
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L  E  R  A  L  L  H  R  A  D  L  P  A  W  M  *  *  A>      140
[P  G  W  K  G  P  Y  C  T  E  P  I  C  L  P  G  C  D  E  Q>]     140
 T  L  A  G  K  G  P  T  A  Q  S  R  S  A  C  L  D  V  M  S>      139

          430        440        450        460        470        480
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I  L  *  Q  T  R  G  M  Q  V  Q  S  G  L  A  G  P  V>      160
[H  G  F  C  D  K  P  G  E  C  K  C  R  V  G  W  Q  G  R  Y>]     160
 S  M  D  F  V  T  N  Q  G  N  A  S  A  E  W  A  G  R  A  G>      159

          490        500        510        520        530        540
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R  V  Y  P  L  S  R  L  S  P  W  H  L  P  A  A  L  A>      180
[C  D  E  C  I  R  Y  P  G  C  L  H  G  T  C  Q  Q  P  W  Q>]     180
 T  V  T  S  V  S  A  I  Q  A  V  S  M  A  P  A  S  S  P  G>      179

          550        560        570        580        590        600
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L  P  G  R  X  G  G  P  F  L  Q  P  G  P  E  L  L  H>      200
[C  N  C  Q  E  G  W  G  G  L  F  C  N  Q  D  L  N  Y  C  T>]     200
 S  A  T  A  R  K  X  G  G  A  F  S  A  T  R  T  *  T  T  A>      199

          610        620        630        640        650        660
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
ACACCATAAG CCCTGCAAGA ATCGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
 T  P  *  A  L  Q  E  W  S  H  L  Q  Q  T  R  A  R  G [S  Y>]      220
[H  H  K  P  C  K  N  G  A  T  C] N  K  H  G  P  G  G  A  T>      220
 H  T  I  S  P  A  R  M  E  P  P  A [T  N  T  G  Q  G] E  L>      219

          670        680        690        700        710        720
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
[T] W  S  L  A  G  L  G  Y  X  G  C  H  L  R  S  L  G  I  G>      240
 L  G  L  W  P  X  W  G  T  X  G  A  T  C  E  A  W  G  L  D>      240
 H  L  V  F  G  R  X  C  V  X  R  V  P  P  A  K  L  G  D  W>      239
```

FIG.12B2

```
      730       740       750       760       770       780
       *   *   *   *   *   *   *   *   *   *   *   *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
R V V D [P S P] W * E R R E L D G S S [E N>]                    260
 E L L T P A L G [K N G G S L T D L] R R T>                     260
T S C * P Q P L V R T E Q A * R I F G E>                        259

      790       800       810       820       830       840
       *   *   *   *   *   *   *   *   *   *   *   *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
[S Y S C T C P P G F Y G K I C E L S A M>]                      280
 A T P V P A H P A S T A K S V N * V P *>                       280
Q L L L Y L P T R L L R Q N L * I E C H>                        279

      850       860       870       880       890       900
       *   *   *   *   *   *   *   *   *   *   *   *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
[T C A D G P C F N G G R C S D S P D G G>]                      300
 P V R T A L A L T G V G A Q T A P M E G>                        300
D L C G R P L L * R G S V L R Q P R W R>                        299

      910       920       930       940       950       960
       *   *   *   *   *   *   *   *   *   *   *   *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
[Y S C R C P V G Y S G F N C E K K I D Y>]                      320
 T A A A A P W A T P A S T V R R K L T T>                       320
V Q L P L P R G L L R L Q L * E E N * L>                        319

      970       980       990       1000      1010      1020
       *   *   *   *   *   *   *   *   *   *   *   *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
[C S S S P C S N G A K C V D L G D A Y L>]                      340
 A A L H P V L M V P S V W T S V M P T C>                        340
L Q L F T L F * W C Q V C G P R * C L P>                        339

      1030      1040      1050      1060      1070      1080
       *   *   *   *   *   *   *   *   *   *   *   *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
[C R C Q A G F S G R H C D D N V D D C A>]                      360
 A A A R P A S R G G T V T T T W T T A P>                        360
V P L P G R L L G E A L * R Q R G R L R>                        359
```

FIG.12B3

```
      1090       1100       1110       1120       1130       1140
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
[S  S  P  C  A  N  G  G  T  C  R  D  G  V  N  D  F  S  C  T>]      380
 P  P  R  A  P  T  G  A  P  A  G  M  A  *  T  T  S  P  A  P>      380
L  L  P  V  R  Q  R  G  H  L  P  G  W  R  E  R  L  L  L  H>      379

      1150       1160       1170       1180       1190       1200
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
[C  P  P  G  Y  T  G  R  N  C  S  A  P  A  S  R  C  E  H  A>]      400
 A  R  L  A  T  R  A  G  T  A  V  P  P  P  A  G  A  S  T  H>      400
L  P  A  W  L  H  G  Q  E  L  Q  C  P  R  Q  Q  V  R  A  R>      399

      1210       1220       1230       1240       1250       1260
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
[P  C  H  N  G  A  T  C  H  E  R  G  H  R  Y] X [C  E  C  A>]      420
 P  A  T  M  G  P  P  A  T  R  G  A  T  A  I  C  A  S  V  P>      420
T  L  P  Q  W  G  H  L  P  R  E  G  P  P  L  F  V  R  V  C>      419

      1270       1280       1290       1300       1310       1320
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
[R  S  Y  G  G  P  N  C] X [F  L  L  P  E] T  A  P  P  A  P>      440
 E  A  T  G  V  P  T  A  X  S  C  S  P  K  L  P  P  R  P  H>      440
P  K  L  R  G  S  Q  L  P  X  P  A  P  R  N  C [P  P  G  P>]      439

      1330       1340       1350       1360       1370       1380
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
 R  W  W  K  L  P  *  K  N  L  K  G  P  G  G  A  H  P  L  G>      460
  G  G  G  N  S  P  K  K  T  *  K  G  R  G  G  P  I  P  L  V>      460
T [V  V] E  T  P  L  K  K  P  K  R  A  G  G  G  P  S  P  W>      459

      1390       1400       1410       1420       1430       1440
       *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
 G  R  V  R  R  G  H  P  C  P  H  A  A  A  G  L  C  R  C  G>      480
  D  V  C  A  G  V  I  L  V  L  M [L  L  L  G  C  A  A  V  V>]     480
W  T  C  A  P  G  S  S  L  S  S  C  C  C  W  A  V  P  L  W>      479
```

FIG.12B4

```
      1450       1460       1470       1480       1490       1500
       *    *     *    *     *    *     *    *     *    *     *    *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
G  L  R  P  A  E  A  A  E  A  P  A  P  S  R  P  L  X  G  C>      500
   V  C  V  R  L  R  L  Q  K  H  R  P  P  A  D  P  X  R  G  E>   500
W  S  A  S  G  *  G  C  R  S  T  G  P  Q  P  T  P  X  G  G>      499

      1510       1520       1530       1540       1550       1560
       *    *     *    *     *    *     *    *     *    *     *    *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
D  C  D  H  E  Q  P  G  Q  L  P  A  *  E  G  H  L  S  Q  H>      520
   T  E  T  M  N  N  L  X  N  C  Q  R  E  K  D  I  S  V  S  I>   520
R  R  R  P  *  T  T  W  X  T  A  S  V  R  R  T  S  Q  S  A>      519

      1570       1580       1590       1600       1610       1620
       *    *     *    *     *    *     *    *     *    *     *    *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
H  R  G  H  A  D  Q  E  H  Q  Q  E  G  G  L  P  R  G  P  Q>      540
   I  G  X  T  Q  I  K  N  T  N  K  K  A  D  F  H  G  D  H  X>   540
S  S  G  X  R  R  S  R  T  P  T  R  R  R  T  S  T  G  T  T>      539

      1630       1640       1650       1660       1670       1680
       *    *     *    *     *    *     *    *     *    *     *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
X  R  Q  E  W  L  Q  G  P  L  P  X  G  G  L  *  P  R  A  G>      560
   A  D  K  N  G  F  K  A  R  Y  P  X  V  D  Y  N  L  V  Q  D>   560
X  P  T  R  M  A  S  R  P  A  T  Q  X  W  T  I  T  S  C  R>      559

      1690       1700       1710       1720       1730       1740
       *    *     *    *     *    *     *    *     *    *     *    *
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
P  Q  G  *  R  H  R  R  Q  G  R  A  Q  Q  A  *  H  Q  V  X>      580
   L  K  G  D  D  T  A  V  R  D  A  H  S  K  R  D  T  K  X  Q>   580
T  S  R  V  T  T  P  P  S  G  T  R  T  A  S  V  T  P  S  X>      579

      1750       1760       1770       1780       1790       1800
       *    *     *    *     *    *     *    *     *    *     *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
A  P  G  L  L  R  G  G  E  G  D  P  R  P  T  L  R  G  W  R>      600
   P  Q  G  S  S  G  E  E  K  G  T  P  D  P  H  S  G  G  G  G>   600
S  P  R  A  P  Q  G  R  R  R  G  P  P  T  H  T  Q  G  V  E>      599
```

FIG.12B5

```
      1810       1820       1830       1840       1850       1860
         *    *     *    *     *    *     *    *     *    *     *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
 K  H  L   E [R  K  R   P] D  F   G  L  V   Q  L [S  K   D] X  Q>   620
  S [I] L   K  E  K   G  R  T [S] G  L  F   N  F  Q   K [T] X  X>   620
E  A  S  *   K  K  K   A  G  L   R  A  C [S  T] F   K  R   Q  X>    619

      1870       1880       1890       1900       1910       1920
         *    *     *    *     *    *     *    *     *    *     *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
 X  T  S   R  C  X   S  F  P   X  E  E   G  *  L   R  H [R  X   L>   640
  V  Q  V   G  V  R   H  F  R   R  R  K   X  D [C  V   I] G  X  *>   640
X  Y  K   S  V  X   V  I  S   X  G  G   R  X  T   A  S  *  E  X>    639

      1930       1940       1950       1960       1970       1980
         *    *     *    *     *    *     *    *     *    *     *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCC GATTCCCNTT TCAAAGTTTT
 R  X  *   X  G  S   *  X  W  K   X  X  P   G  F  R   F  Q  S  F>   660
  G  X  K   X  X  V   X  X  G  K   X  S  P   D  S  X   F  K  V  F>   660
[E  V] V   X  W  X   L  X  L  E   X  X  P   R  I  P   X  S  K  F>    659
```

FIG.12B6

```
MOUSE DELTA DNA  GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50
HUMAN DELTA      ---------- ---------- ---------- ---------- ----------

CONSENSUS        GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50

MOUSE DELTA DNA  CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100
HUMAN DELTA      ---------- ---------- ---------- ---------- ----------

CONSENSUS        CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100

MOUSE DELTA DNA  CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150
HUMAN DELTA      ---------- ---------- ---------- ---------- ----------

CONSENSUS        CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150

MOUSE DELTA DNA  CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200
HUMAN DELTA      ---------- ---------- ---------- ---------- ----------

CONSENSUS        CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200

MOUSE DELTA DNA  TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250
HUMAN DELTA      ---------- ---------- ---------- ---------- ----------

CONSENSUS        TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250

MOUSE DELTA DNA  AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGC  300
HUMAN DELTA      ---------- ---------- ---------- ---------- -----CATTG    5

CONSENSUS        AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTSATKG  300

MOUSE DELTA DNA  CGCAGGCATC GACCGC---G CCTTCAGCAA CCCCA--TCC GAT-TC-CCC  343
HUMAN DELTA      GGTACGGGCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT   55

CONSENSUS        SGYASGSRYC SMCCYCGAGG YCKWCRGYAW CSMYAAGYYY GATATCGMMY  350

MOUSE DELTA DNA  TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCCTCCA  393
HUMAN DELTA      TCCGGCTTCA CCTGGCCGGG CACCTTCTCT CTGATTATTG AAGCTCTCCA  105

CONSENSUS        TYCGGCTTCA CCTGGCCRGG YACCTTCTCT CTGATYATTG AAGCYCTCCA  400

MOUSE DELTA DNA  TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  443
HUMAN DELTA      CACAGATTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  155

CONSENSUS        YACAGAYTCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  450
```

FIG.13A

```
MOUSE DELTA DNA GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGAGAAGA ATGGTCTCAG  493
HUMAN DELTA     GCCGCCTGGC CACCCAGAGG CACCTGACGG TGGGCGAGGA GTGGTCCCAG  205

CONSENSUS       GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGMGARGA RTGGTCYCAG  500

MOUSE DELTA DNA GACCTTCACA GTAGCGGCCG CACAGACCTC CGGTACTCTT ACCGCTTTGT  543
HUMAN DELTA     GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT  255

CONSENSUS       GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT ACCGSTTYGT  550

MOUSE DELTA DNA GTGTGACGAG CACTACTACG GAGAAGGTTG CTCTGTCTTC TGCCGACCTC  593
HUMAN DELTA     GTGTGACGAA CACTACTACG GAGAGGGCTG CTCCGTTTTC TGCCGTCCCC  305

CONSENSUS       GTGTGACGAR CACTACTACG GAGARGGYTG CTCYGTKTTC TGCCGWCCYC  600

MOUSE DELTA DNA GGGATGACGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG  643
HUMAN DELTA     GGGACGATGC CTTCGGCCAC TTCACCTGTG GGGAGCGTGG GGAGAAAGTG  355

CONSENSUS       GGGAYGAYGC CTTYGGCCAC TTCACCTGYG GGGASMGWGG GGAGAARRTG  650

MOUSE DELTA DNA TGCGACCCTG GCTGGAAAGG CCAGTACTGC GCTGACCCAA TCTGTCTGCC  693
HUMAN DELTA     TGCAACCCTG GCTGGAAAGG GCCCTACTGC ACAGAGCCGA TCTGCCTGCC  405

CONSENSUS       TGCRACCCTG GCTGGAAAGG SCMSTACTGC ACWGASCCRA TCTGYCTGCC  700

MOUSE DELTA DNA AGGGTGTGAT GACCAACATG GATACTGTGA CAAACCAGGG GAGTGCAAGT  743
HUMAN DELTA     TGGATGTGAT GAGCAGCATG GATTTTGTGA CAAACCAGGG GAATGCAAGT  455

CONSENSUS       WGGRTGTGAT GASCARCATG GATWYTGTGA CAAACCAGGG GARTGCAAGT  750

MOUSE DELTA DNA GCAGAGTTGG CTGGCAGGGC CGCTACTGCG ATGAGTGCAT CCGATACCCA  793
HUMAN DELTA     GCAGAGTGGG CTGGCAGGGC CGITACTGTG ACGAGTGTAT CCGCTATCCA  505

CONSENSUS       GCAGAGTKGG CTGGCAGGGC CGSTACTGYS AYGAGTGYAT CCGMTAYCCA  800

MOUSE DELTA DNA GGTTGTCTCC ATGGCACCTG CCAGCAACCC TGGCAGTGTA ACTGCCAGGA  843
HUMAN DELTA     GGCTGTCTCC ATGGCACCTG CCAGCAGCCC TGGCAGTGCA ACTGCCAGGA  555

CONSENSUS       GGYTGTCTCC ATGGCACCTG CCAGCARCCC TGGCAGTGYA ACTGCCAGGA  850

MOUSE DELTA DNA AGGCTGGGGG GGCCTTTTCT GCAACCAAGA CCTGAACTAC TGTACTCACC  893
HUMAN DELTA     AGGNTGGGGG GGCCTTTTCT GCAACCAGGA CCTGAACTAC TGCACACACC  605

CONSENSUS       AGGNTGGGGG GGCCTTTTCT GCAACCARGA CCTGAACTAC TGYACWCACC  900
```

FIG.13B

```
MOUSE DELTA DNA ATAAGCCGTG CAGGAATGGA GCCACCTGCA -CCAACACGG GCCAGGGG-A  941
HUMAN DELTA     ATAAGCCCTG CAAGAATGGA GCCACCTGCA ACAAACACGG GCCAGGGGGA  655

CONSENSUS       ATAAGCCSTG CARGAATGGA GCCACCTGCA ACMAACACGG GCCAGGGGGA  950

MOUSE DELTA DNA GCTACACATG TTCCT-GCC -GACCTGGGT ATACA-GGTG CCAACTGTG-  986
HUMAN DELTA     GCTACACTTG GTCTTTGGCC GGNCTGGGGT ACANAGGGTG CCACCTGCGA  705

CONSENSUS       GCTACACWTG KTCYTTGGCC GGNCYKGGGT AYANAGGGTG CCAMCTGYGA 1000

MOUSE DELTA DNA AGCT-GGAA GTAGATGAG- TG-TGCTCCT AGCCCCT-GC AAGAACGGAG 1031
HUMAN DELTA     AGCTTGGGGA TTGGACGAGT TGTTGACCCC AGCCCTTGGT AAGAACGGAG  755

CONSENSUS       AGCTTGGGRA KTRGAYGAGT TGTTGMYCCY AGCCCYTGGY AAGAACGGAG 1050

MOUSE DELTA DNA CGAGCTGCAC GGACCTT-G AGGACAGCTT CTCTTGCACC TGCCCTCCCG 1079
HUMAN DELTA     GGAGCTTGAC GGATCTTCGG AGAACAGCTA CTCCTGTACC TGCCCACCCG  805

CONSENSUS       SGAGCTKSAC GGAYCTTCGG AGRACAGCTW CTCYTGYACC TGCCCWCCCG 1100

MOUSE DELTA DNA GCTTCTATGG CAAGGTCTGT GAGCTGAGCG CCATGACCTG TGCAGATGGC 1129
HUMAN DELTA     GCTTCAACGG CAAAATCTGT GAATTGAGTG CCATGACCTG TGCGGACGGC  855

CONSENSUS       GCTTCTAYGG CAARRTCTGT GARYTGAGYG CCATGACCTG TGCRGAYGGC 1150

MOUSE DELTA DNA CCTTGCTTCA ATGGAGGACG ATGTTCAGAT AACCCTGACG GAGGCTACAC 1179
HUMAN DELTA     CCTTGCTTTA ACGGGGGTCG GTGCTCAGAC AGCCCCGATG GAGGCTACAG  905

CONSENSUS       CCTTGCTTYA AYGGRGGWCG RTGYTCAGAY ARCCCYGAYG GAGGSTACAS 1200

MOUSE DELTA DNA CTGCCATTGC CCCTTGGGCT TCTCTGGCTT CAACTGTGAG AAGAAGATGG 1229
HUMAN DELTA     CTGCCGCTGC CCCGTGGGCT ACTCCGGCTT CAACTGTGAG AAGAAAATTG  955

CONSENSUS       CTGCCRYTGC CCCKTGGGCT WCTCYGGCTT CAACTGTGAG AAGAARATKG 1250

MOUSE DELTA DNA ATCTCTGCGG CTCTTCCCCT TGTTCTAACG GTGCCAAGTG TGTGGACCTC 1279
HUMAN DELTA     ACTACTGCAG CTCTTCACCC TGTTCTAATG GTGCCAAGTG TGTGGACCTC 1005

CONSENSUS       AYYWCTGCRG CTCTTCMCCY TGTTCTAAYG GTGCCAAGTG TGTGGACCTC 1300

MOUSE DELTA DNA GGCAACTCTT ACCTGTGCCG CTGCCAGGCT GGCTTCTCCG GGAGGTACTG 1329
HUMAN DELTA     GGTGATGCCT ACCTGTGCCG CTGCCAGGCC GGCTTCTCGG GGAGGCACTG 1055

CONSENSUS       GGYRAYKCYT ACCTGTGCCG CTGCCAGGCY GGCTTCTGSG GGAGGYACTG 1350

MOUSE DELTA DNA CGAGGACAAT GTGGATGACT GTGCCTCCTC CCCGTGTGCA AATGGGGGCA 1379
HUMAN DELTA     TGACGACAAC GTGGACGACT GCGCCTCCTC CCCGTGCGCC AACGGGGGCA 1105

CONSENSUS       YGASGACAAY GTGGAYGACY GYGCCTCCTC CCCGTGYGCM AAYGGGGGCA 1400
```

FIG.13C

MOUSE DELTA DNA	CCTGCCGGGA CAGTGTGAAC GACTTCTCCT GTACCTGCCC ACCTGGCTAC	1429
HUMAN DELTA	CCTGCCGGGA TGGCGTGAAC GACTTCTCCT GCACCTGCCC GCCTGGCTAC	1155
CONSENSUS	CCTGCCGGGA YRGYGTGAAC GACTTGTCCT GYACCTGCCC RCCYGGCTAC	1450
MOUSE DELTA DNA	ACGGGCAAGA ACTGCAGCGC CCCTGTCAGC AGGTGTGAGC ATGCACCCTG	1479
HUMAN DELTA	ACGGGCAGGA ACTGCAGTGC CCCCGCCAGC AGGTGCGAGC ACGCACCCTG	1205
CONSENSUS	ACGGGCARGA ACTGCAGYGC CCCYGYCAGC AGGTGYGAGC AYGCACCCTG	1500
MOUSE DELTA DNA	CCATAATGGG GCCACCTGCC ACCAGAGGGG CCAGCGCTAC ATGTGTGAGT	1529
HUMAN DELTA	CCACAATGGG GCCACCTGCC ACGAGAGGGG CCACCGCTAT TTGTGCGAGT	1255
CONSENSUS	CCAYAATGGG GCCACCTGCC ACSAGAGGGG CCASCGCTAY WTGTGYGAGT	1550
MOUSE DELTA DNA	GCGCCCAGGG CTATGGCGGC CCCAACTGCC AGTTTCTGCT CCCTG-AGCC	1578
HUMAN DELTA	GTGCCCGAAG CTACGGGGGT CCCAACTGCC ANTTCCTGCT CCCCGAAACT	1305
CONSENSUS	GYGCCCRRRG CTAYGGSGGY CCCAACTGCC ANTTYCTGCT CCCYGAARCY	1600
MOUSE DELTA DNA	-ACCACCAGG GCCCATGGTG GTGG-ACCTC AGTGAGAGGC ATAT-GGAGA	1625
HUMAN DELTA	GCCCCCCCGG CCCCACGGTG GTGGAAACTC CCCTAAAAAA ACCTAAAAGG	1355
CONSENSUS	GMCCMCCMGG SCCCAYGGTG GTGGAAMCTC MSYKARARRM AYMTARRAGR	1650
MOUSE DELTA DNA	GCCAGGGCGG GCCCTTCCCC TGGGTGGCCG TGTGTGCCGG GGTGGTGCTT	1675
HUMAN DELTA	GCCGGGGGGG GCCCATCCCC TTGGTGGACG TGTGCGCCGG GGTCATCCTT	1405
CONSENSUS	GCCRGGGSGG GCCCWTCCCC TKGGTGGMCG TGTGYGCCGG GGTSRTSCTT	1700
MOUSE DELTA DNA	GTCCTCCTGC TGCTGCTGGG CTGTGCTGCT GTGGTGGTCT GCGTCCGGCT	1725
HUMAN DELTA	GTCCTCATGC TGCTGCTGGG CTGTGCCGCT GTGGTGGTCT GCGTCCGGCT	1455
CONSENSUS	GTCCTCMTGC TGCTGCTGGG CTGTGCYGCT GTGGTGGTCT GCGTCCGGCT	1750
MOUSE DELTA DNA	GAAGCTACAG AAACACCAGC CTCCATCTGA ACCCTGTGGG GGAGAGACAG	1775
HUMAN DELTA	GAGGCTGCAG AAGCACCGGC CCCCATCCGA CCCCTGNCGG GGGGAGACGG	1505
CONSENSUS	GARGCTRCAG AARCACCRGC CYCCASCYGA MCCCTGNSGG GGRGAGACRG	1800
MOUSE DELTA DNA	AAACCATGAA CAACCTAGCC AATTGCCAGC GCGAGAAGGA CGTTTCTGTT	1825
HUMAN DELTA	AGACCATGAA CAACCTGGNC AACTGCCAGC GTGAGAAGGA CATCTCAGTC	1555
CONSENSUS	ARACCATGAA CAACCTRGNC AAYTGCCAGC GYGAGAAGGA CRTYTCWGTY	1850

FIG.13D

```
MOUSE DELTA DNA AGCATCATTG GGGCTACCCA GATCAAGAAC ACCAACAAGA AGGCGGACTT 1875
HUMAN DELTA     AGCATCATCG GGGNCACGCA GATCAAGAAC ACCAACAAGA AGGCGGACTT 1605

CONSENSUS       AGCATCATYG GGGNYACSCA GATCAAGAAC ACCAACAAGA AGGCGGACTT 1900

MOUSE DELTA DNA TCACGGGGAC CATGGAGCCA AGAAGAGCAG CTTTAAGGTC CGATACCCCA 1925
HUMAN DELTA     CCACGGGGAC CACAGNGCCG ACAAGAATGG CTTCAAGGCC CGCTACCCAG 1655

CONSENSUS       YCACGGGGAC CAYRGNGCCR ASAAGARYRG CTTYAAGGYC CGMTACCCMR 1950

MOUSE DELTA DNA CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACGGTC 1975
HUMAN DELTA     NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGACGA CACCGCCGTC 1705

CONSENSUS       NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGWGAYGA MRCCRCSGTC 2000

MOUSE DELTA DNA AGGGATACAC ACAGCAAACG TGACACCAAG TGCCAGTCAC AGAGCTCTGC 2025
HUMAN DELTA     AGGGACGCGC ACAGCAAGCG TGACACCAAG TGNCAGCCCC AGGGCTCCTC 1755

CONSENSUS       AGGGAYRCRC ACAGCAAFCG TGACACCAAG TGNCAGYCMC AGRGCTCYKC 2050

MOUSE DELTA DNA AGGAGAAGAG AA---GATCG CC--CCAACA CTTA-GGGGT GG-GG-AGAT 2067
HUMAN DELTA     AGGGGAGGAG AAGGGGACCC CCGACCCACA CTCAGGGGGT GGAGGAAGCA 1805

CONSENSUS       AGGRGARGAG AAGGGGAYCS CCGACCMACA CTYAGGGGGT GGAGGAAGMW 2100

MOUSE DELTA DNA TCCTGACAGA AAAAGGCCAG AGTCT--GTC TACTCTAC-T TCAAAGGAC- 2113
HUMAN DELTA     TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCAACTT TCAAAAGACA 1855

CONSENSUS       TCYTGAMAGA AAAAGGCCRG ASTYYGGGYY TRYTCWACTT TCAAARGACA 2150

MOUSE DELTA DNA -ACCAAGTAC CAGTCGGTGT ATGTTCTGTC TGCAGAA--A AGGATGAGTG 2160
HUMAN DELTA     ANCAANGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGGA AGGNTGACTG 1905

CONSENSUS       ANCMANGTAC MAGTCGGTGT NYGTYMTKTC YGNAGRAGGA AGGNTGASTG 2200

MOUSE DELTA DNA TGTTATA-GC GACTGAGGT- GTAAGATGGA AGCGATGTGG CAAAATTCCC 2208
HUMAN DELTA     CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG---T-TG- --ANNTT-- 1945

CONSENSUS       YGTYATAGGM RNYTGAGCTN GTAARNTGGN AGCGATGTGG CAANNTTCCC 2250

MOUSE DELTA DNA ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTGCTGA 2258
HUMAN DELTA     -------GGA AAGNNN- TC CCCGGAT--- --TCCGNT-- ----TTC--- 1972

CONSENSUS       ATTTCTCKSA AAKNNNATTC CMMGGATATA GCYCCGNTGA ATGCTKCTGA 2300
```

FIG.13E

```
MOUSE DELTA DNA GAGAGGAAGG GAGAGGAAAC CCAGGGACTG CTGCTGAGAA CCAGGTTCAG  2308
HUMAN DELTA     ---------- ------AAA- ---------G TTTTT----- ----------  1981

CONSENSUS       GAGAGGAAGG GAGAGGAAAC CCAGGGACTG YTKYTCAGAA CCAGGTTCAG  2350

MOUSE DELTA DNA GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2358
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT  2400

MOUSE DELTA DNA AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2408
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG  2450

MOUSE DELTA DNA GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2458
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA  2500

MOUSE DELTA DNA TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2508
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA  2550

MOUSE DELTA DNA GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2558
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC  2600

MOUSE DELTA DNA TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2608
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT  2650

MOUSE DELTA DNA TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2658
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT  2700

MOUSE DELTA DNA ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2708
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA  2750
```

FIG.13F

```
MOUSE DELTA DNA AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT  2758
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT  2800


MOUSE DELTA DNA ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA  2808
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA  2850

MOUSE DELTA DNA AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA   2857
HUMAN DELTA     ---------- ---------- ---------- ---------- ----------  1981

CONSENSUS       AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA   2899
```

FIG.13G

GFTWPGTFSLIIEALHTDSPD> 21

DLATENPERLISRLATQRHL> 41

TVGEEWSQDLHSSGRIDLKY> 61

SYRFVCDEHYYGEGCSVFCR> 81

PRDDAFGHFTCGERGEKVCN> 101

PGWKGPYCTEPICLPGCDEQ> 121

HGFCDKPGECKCRVGWQGRY> 141

CDECIRYPGCLHGTCQQPWQ> 161

CNCQEGWGGLFCNQDLNYCT> 181

HHKPCKNGATC*TNTGQG* 198

SYT*PSP*KNGGSLTDL* 213

ENSYSCTCPPGFYGKICELSAM> 235

TCADGPCFNGGRCSDSPDGG> 255

YSCRCPVGYSGFNCEKKIDY> 275

CSSSPCSNGAKCVDLGDAYL> 295

CRCQAGFSGRHCDDNVDDCA> 315

SSPCANGGTCRDGVNDFSCT> 335

CPPGYTGRNCSAPASRCEHA> 355

PCHNGATCHERGHRY*CECA> 374

RSYGGPNC*FLLPE*PPGP*> 391

VV*LLLGCAAVVVCVRLRLQKH> 412

RPPADP*RGETETMNNL*> 428

FIG. 14A

NCQREKDISVSIIG*TQIKNTN> 449

KKADFHGDH*ADKNGFKARYP* 469

VDYNLVQDLKGDDTAVRDAHSKRDTK* 494

QPQGSSGEEKGTP*PTLR*GG* 514

I*RKRP*S*ST*SKD*T* 526

CVI*EV* 531

FIG. 14B